



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/892,316

DATE: 05/30/2003

TIME: 12:18:52

Input Set : N:\Crf3\RULE60\09892316.RAW.txt
Output Set: N:\CRF4\05302003\I892316.raw

SEQUENCE LISTING

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62	20	25	30	
63	His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Pro Asp Gln			
64	35	40	45	
65	Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg			
66	50	55	60	
67	Trp Ala Glu Arg Leu Phe Pro Ala Asn Val Ala His Ser Val Tyr Val			
68	65	70	75	80
69	Leu Glu Asp Ser Ile Val Asp Pro Gln Asn Gln Thr Met Thr Thr Phe			
70	85	90	95	
71	Thr Trp Asn Ile Asn His Ala Arg Leu Met Val Val Glu Glu Arg Cys			
72	100	105	110	
73	Val Tyr Cys Val Asn Ser Asp Asn Ser Gly Trp Thr Glu Ile Arg Arg			
74	115	120	125	
75	Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln			
76	130	135	140	
77	Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Thr Met Lys			
78	145	150	155	160
79	Gly Phe Glu Tyr Ile Leu Ala Lys Leu Gln Gly Glu Ala Pro Ser Lys			
80	165	170	175	
81	Thr Leu Val Glu Thr Ala Lys Glu Ala Lys Glu Lys Ala Lys Glu Thr			
82	180	185	190	
83	Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala			
84	195	200	205	
85	Thr Lys Lys Gln Gln Gln Gln Phe Val			
86	210	215		

88 (2) INFORMATION FOR SEQ ID NO: 2:

90 (i) SEQUENCE CHARACTERISTICS:
 91 (A) LENGTH: 858 base pairs
 92 (B) TYPE: nucleic acid
 93 (C) STRANDEDNESS: single
 94 (D) TOPOLOGY: linear

97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

99	GC GG GT GG TG A CTG AG GCT TAC G AG C CT GG CG G CG GG GT GT CG C CG AG C C C C G G C C C G	60
100	G C C C T C G C G T G C C T C G C C A C C C T G A T G C T G C G C G G G T G C T G A G C C C G C T T C	120
101	G G C C G G G A C G A T G G T G A A G T A T T C C T G G G C C A G A G C G T G C T C C G G A G T T C C T G G G A C C A	180
102	A G T G T T C G C C G C C T C T G G C A G C G G T A C C C G A A T C C C T A T G C A A A C A T G T C T G A C G G A	240
103	A G A C A T A G T A C A C C G G G A G G T G A C C C C T G A C C G A A C A T G C T G T C C C G G C G A C T C C T G A C	300
104	C A A G A C C A A C A G G A T G C C A C G C T G G G C C G A G C A C T A T T T C C T G C C A A T G T T G C T C A C T C	360
105	G G T G T A C G T C C T G G A G G A C T C T A T T G T G G A C C C A C A G A A T C A G A C C A T G A C T A C T T C A C	420
106	C T G G A A C A T C A A C C A C G C C C G G C T G A T G G T G G T G G A G G A C G A T G T G T T T A C T G T G T G A A	480
107	C T C T G A C A A C A G T G G C T G G A C T G A A T C C G C C G G G A A G G C T G G T C T C C T C T A G C T T A T T	540
108	T G G T G T C T C C A G A G C T G T C C A G G A A T T G G T C T G C C C G G T T C A A A A G C A A C G T G A C C A A	600
109	G A C T A T G A A G G G T T T G A A T A T C T T G G C A A G G C A G G C C C C T T C C C A A A A C	660
110	A C T T G T T G A G A C A G C C A A G G A A G G C C A A G G A G A G C G G C A C T G G C A G G C T A C	720
111	A G A G A A G G G C C A G G A C C T C G C C A G C A A G G C G G C A C C A A G A A G C A G C A G C A G C A A C A	780
112	G T T T G T G T A G C C A G T C T A C C A C C A C A G C A C C C A G A C A G C T T A G G C T T A G G C T T A G G C T T	840
113	C C C T C C C T T C A T T G T A C T	858

115 (2) INFORMATION FOR SEQ ID NO: 3:

117 (i) SEQUENCE CHARACTERISTICS:

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118 (A) LENGTH: 215 amino acids
119 (B) TYPE: amino acid
120 (C) STRANDEDNESS: single
121 (D) TOPOLOGY: linear
123 (vii) IMMEDIATE SOURCE:
124 (A) LIBRARY: GenBank
125 (B) CLONE: 969170
127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
129 Met Gly Lys Tyr Cys Ala Ser Leu Gly Val Leu Lys Gly Pro Trp Asp
130 1 5 10 15
131 Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys
132 20 25 30
133 His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Ala Asp His
134 35 40 45
135 Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg
136 50 55 60
137 Trp Ala Glu Arg Phe Phe Pro Ala Asn Val Ala His Asn Val Tyr Ile
138 65 70 75 80
139 Val Glu Asp Ser Ile Val Asp Pro Lys Asn Arg Thr Met Thr Phe
140 85 90 95
141 Thr Trp Asn Ile Asn His Ala Arg Leu Met Ala Val Glu Glu Arg Cys
142 100 105 110
143 Val Tyr Arg Val Asn Pro Glu Asn Ser Ser Trp Thr Glu Val Lys Arg
144 115 120 125
145 Glu Ala Trp Val Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln
146 130 135 140
147 Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Ser Thr Lys
148 145 150 155 160
149 Gly Phe Glu Tyr Val Leu Ala Arg Met Gln Gly Glu Ala Pro Ser Lys
150 165 170 175
151 Thr Leu Val Glu Thr Ala Lys Glu Ala Thr Glu Lys Ala Lys Glu Thr
152 180 185 190
153 Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala
154 195 200 205
155 Thr Lys Lys Lys Gln Phe Val
156 210 215

VERIFICATION SUMMARY
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]